

Online Supplementary Data 4

Phylogeny and paleobiogeography of Hegetotheriidae (Mammalia, Notoungulata)

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RH: SEOANE *ET AL.*—PHYLOGENY AND PALEOBIOGEOGRAPHY OF  
HEGETOTHERIIDAE

Journal of Vertebrate Paleontology

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## DETECTED PROBLEMS OF RASP 3.2, BAYESIAN METHOD

### Alphabetical Probability

One of the problems of this method is the assignation of higher probabilities in accordance to alphabetic order. This causes that for two areas that have the same probability of being the ancestral area, the program gives a higher probability to the area identified with the letter that is first in the alphabetical order.

With an easy example, we can clearly see the procedure of the program. We want to determine the ancestral area in a clade of three species, whose relations are (sp 1, (sp 2 + sp 3)) (Fig. 1S). Species 2 and 3 are in areas A and B, whereas species 1 is in area C (Table 1S). The Figure 2S shows the result of the Bayesian Analysis in RASP (Samplefreq = 100; ngen = 50,000; nchains = 10; Temp = 0.1). We observe that the ancestral area assigned to node 1 is A, with 99.55% Bayesian support. Even if the analysis is more exhaustive (Samplefreq = 1000; ngen = 1,000,000; nchains = 20; Temp = 0.1), the area A remains as the most probable area (99.54%) and area B is not considered.

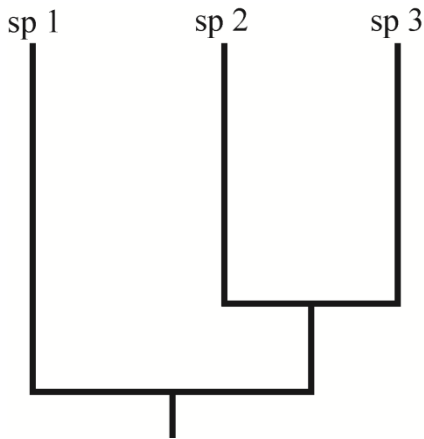


Figure 1S. Phylogenetic relationships of three hypothetical species.

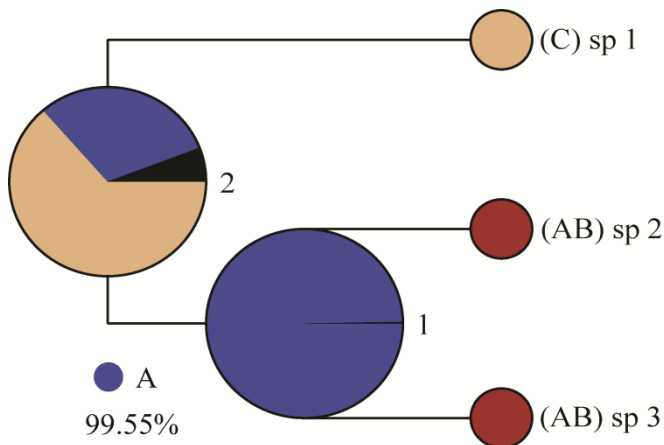


Figure 2S. Result of Bayesian analysis. Node 1 with 99.55% Bayesian support to the area A and not considering area B.

Table 1S. Species and areas where they are found.	
Species	Areas
1	C
2	AB
3	AB

### Extra Dispersive Events

Other problem detected in the Bayesian method is the consideration of dispersive events when there is no biogeographic meaning for them. In our analysis in particular, we advertise that the program generates extra dispersive events in some nodes. For example, the node 38 in Figure 3S represents the postdesadan Pachyrukhinae clade and the ancestor is represented in areas IJ. Likewise, the child nodes 37, 36 and 34 as well the child taxon (*Paedotherium bonaerense*) have the same distribution (IJ). Therefore, there should not be any dispersion, because both the ancestor and the descendants inhabit the same areas, but the program resolves both nodes (38 and 37) with two dispersal events each (Table 6).

This error was detected 14 times in the biogeographic analysis of Hegetotheriidae (see main text) and it is not known yet why this problem happens.

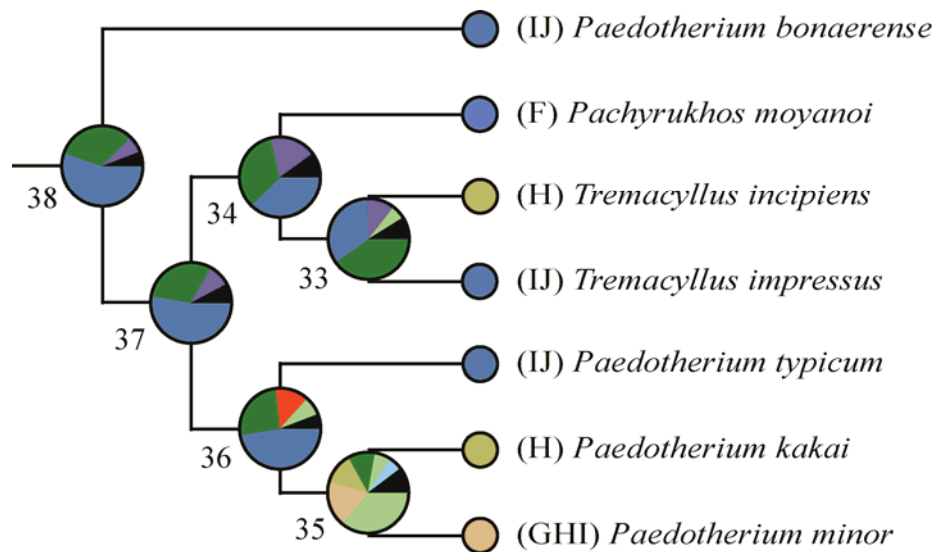


Figure 3S. Result of Bayesian analysis of family Hegetotheriidae (see main text). Nodes 38, 37, 36 and 34 with IJ as ancestral area.

### CONCLUSION

Solving these detected problems would allow obtaining more accurate probability values concerning the assignation of ancestral areas, and would avoid the generation of extra dispersive events in the analysis.